

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGC~~GGG~~GCTGCTAGGCCTC
TGTGCCGGGCTTGGATT CGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATGCCCGGC
GTTTGGCCAGGACGGGCCATGTGGTCGT CAGCAGCCGAAGCAGCAGAATGTGGACCAAG
GCGGTGGCCACGCTGCAGGGGAGGGCTGAGCGTGACGGCACCGTGTGCCATGTGGGAA
GGCGGAGGACCGGGAGCGGCTGGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCTTCTTGGAAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTATCGTCTTCCATAGCAGCCTCAGTC
CATCTCCTGGCTTCAGTCCTACAATGTCAGTAAAACAGCCTGCTGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTACAA
GAAGCTTCAGCAGGATGCTGGATGGACAAGGAAAAGAGGAAAGCATGAAAGAAACCC
TGCAGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTCTTCCCTGTCT
GAAGATGCCAGCTACATCACTGGGAAACAGTGGTGGTGGTGGAGGAACCCGCC
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGCTCTAGCTCCTGGCTGTTCTGC
ATTCAACCACTGGCTTCCCACCTCTGCTCACCTTACTGTTCACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTCCCTGCCGTCAAGGTGGCGTCTACTCGGGATTCCCTGCT
GTTGTTGTGGCCTTGGTAAAGGCCTCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTCCGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAACCTGGAGTGGAGGAGCAGAGTTGCAAATTAAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTGAAAAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLIRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

FIGURE 4

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465
<subunit 1 of 1, 830 aa, 1 stop
<MW: 95029, pI: 8.26, NX(S/T): 2
MEQYKLQSDRLREQQEEMVELRLRLELVRPGWGLRLLNGLPPGSFVPRPHTAPLGGAHAV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPELCLEELDAI PGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRRLREETEQKRRLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVSLEQQQKIEEQQKWLQEMEKVLQQRRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAQSQQQIRGEIDS
LRQEKDSSLKQRLEIDGKLRQGSLLSPEEERTLFQLDEAIEALDAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLQQSRDHLGEGLADSRRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTTREETRDLVHAPLPLTWKRSSLGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL
```

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTGGAAAGCATGAGGCCACGATGCTGCATCTGGCTTGTCTGCT
GGATAACAGTCTCCTCCTCCAGTGTCAAAAGGAACTACAGACGCTCCTGGCTCAGGA
CTGTGGCTGTGCCAGCGACACCCAGGTGTGGAAACAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTGAGCTCTGCTGTCCCAGTCTTGGCCCCCAGCAGAAGTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCCTAAAAACCCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTGGAGAGGAGCCCAGCTGGGATGGC
CAGACTTCAGGGGAAGAATGCCTCCTGCTTCATCCCTTCCAGCTCCCTCCCGCTGAG
AGCCACTTCACGGCAATAAAATCCCCCACATTACCATCT

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRLGMKSQCHLSPISRCSRNRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCCACGCGTCCGCCAACGCGTCCGGTGCCACTCGCGCCGGCGCTCCGGCTTCTCT
TTTCCCTCCGACGCCACGGCTGCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCCCTCCGGAGAGGGAGCGAGGCCGGAGGATGAGCGACTGAGGGCGACGCCGGCACTGACGCGAGTT
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCCGGCACTGACGCGAGTT
GGGGCCCGCACTACCGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCG
GTGTGCGCGCCAGGCGAGCGCGCAGGTGGGCTGGCTTTAGTGGTCCGCCAACGCCGG
TCGCCGGCCGGCCAGGATGGCGCTGGCAACCCGGCCGCCGCGCTGCTACCCCTG
CGCCCGCTGCGAGCCCGCGTCCGGCCCGCCCTGCGCTCATGGACGGCGCTCCCGCTG
GCCGGCGCGCCGGCTGTGAATGCGACTGCCCTCGGCCGCTCCCGCCGCC
GCCCGCCGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCCTGGTCACCTGCTGCCGTGGCTCTGTGCAGTCGAGCATCCGCTGGAG
AAGCTGGCCAGGCACCAGAGCAGCCGGCCAGGAGAACGCGTGAGCACGCCACTCGGACGG
CCCGGGCGGGTGAACGAGCTCGGCGCCGGCGAGGGACGAGGGCGGAGCGGCCGGACT
GGAAGAGCAAGAGCGGCCGTGGCTGCCGGCGTGAGCCGTGGAGAACGCTGAAGCAGGCC
TGGGTCTCCCAGGGCGGGGGGCCAACGCCGGGATCTGCAGGTCCGCCCGCGGGACAC
CCCGCAGGCCGAAGCCCTGCCGCAGCCGCCAGGACGCGATTGCCCGGAACCGCC
CGCCCGAGCCACCCGAGGAGTACGTGTACCGGACTACCGTGGCAAGGGCTGCGTGAG
AGCGGCTCGTGTACCGATCGGGAGAACGTTCGCCGCCCTCGCCTGCCGTGCCT
GTGCACCGAGGAGGGCCGCTGTGCGCGAGCCGAGTGCCCGAGGCTGCACCGCGCTGCA
TCCACGTCGACACGAGCCAGTGCCTGCCCGAGTCAAGGAGAGAACACTACTGCGAGTT
CGGGCAAGACCTATCAGACTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTCAAGCGTGTCCCAGACGGAGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCCTGCCATCTGCAAAATGGTCAAACACTGCTTGCAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAACGAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAACGAGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATGTAGACGCTTCCAGAACACAAACTCTGACTTTCTAGAACATTTACTGATGTGAA
CATTCTAGATGACTCTGGAACTATCAGTCAAAGAACGACTTTGATGAGGAATAATGGAAAA
TTGTTGGTACTTTCTTCTTGATAACAGTTACTACAACAGAACGAGGAAATGGATATATT
AAAACATCAACAAGAACCTTGGCATAAAATCCTCTAAATAATGTGCTATTTCACAG
TAAGTACACAAAAGTACACTATTATATCAAATGTATTCTATAATCCCTCATTAGAGAG
CTTATATAAGTGTCTATAGATGCAGATTAAAATGCTGTGCAACCGTCAAAAAAA
AAAAAAAAAAAAAAAAAA

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSLLVTCLMVALCSPSIPLEKLAQAPEQPGQEKRHATRDGPGRVNEL
GRPARDEGGSGRDWKSKGRLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALA
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDESGFVYAIKEKFAPGPSACPCLCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGT**A**TGAGCGCGGTATTACTGCTGGCCCTCCTGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTGGACAGTCAGCATGTGTGGAAAGGTGTCC
GACCTACCCGGCAATGGACCCCTAAGAACACCAAGCTGCACAGCGGCTTGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCAAGTGAGCCTGGTCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCCGCGTCACTGAGCACCGATGGGCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAAACCTCGTTAACCTCCCTCCGCT
TTGGGCCACAGCCCCCAGCAGACCCAGGATCCTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGACAACAGAAAGAGATCTGCCCAAGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTCTGACCTGTCATCGGGGACCACCATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
GTGTCAGGAGACGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGACAAAAG
GCTGCAGCACTGTTGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACCGCAGTGTG
CTACCTGTGTGCAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGCTGTCCACCAAAAT
GAGCATTCAAGGCTGCGTGGCCAACCTCCAGCTTGAACCACACCAGACAAATCG
GGATCTCTCTGCGCGTGAGAACGCTGATGTGCAAGCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGACTGGCCACTGGCCCCAGCGCTGTG
GTGGGAGTGGTTGCCCTCCTGCT**AA**CTCTATTACCCCCACGATTCTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTGACCTCATAACCTAATGGCCTGGACACCAGATTCTTC
CCATTCTGTCCATGAATCATCTCCCCACACACAATCATTCAATCTACTCACCTAACAGCA
ACACTGGGAGAGCCTGGAGCATCCGGACTTGCCTATGGGAGAGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCTTCA

FIGURE 10

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><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTTEEICPKGTTCYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPGVGMTECNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGPKGCTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACG**A**TGCTACGCGGCCGGCTGCCTCCGTAGCGCTGCCGCCCTG
GCTGCGCGCTGCTCTCGCTTGCACGGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGC
CTCGTCGCTCAGCCCTATTCGGCACCAAGACTCGCTACGAGGATGTCAACCCGTGCTAT
TGTGGGCCCCGAGGCTCCGTGGGGACCCCTGAGCTGCTGGAGGGACCTGCACCCGGT
CAGCTGGTCGCCCTCATCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGTTGCTGCAGGCCGCGGGTCCAGGGATGGCGGGCTAGTAGTACCG
GCAGCCCGACCTGGGTGCAGCGCTGGCGACTGGCCTTGTGGTACCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGCTGGCCTCGCT
CTTCCCGCCCTTTCAGCGTGAGAACTACGCCGCTGCGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCCTCCTGCAGGGCTGTGGCAGCAGTACCAACCCCTGGC
TTGCCGCCGGACGTCGCAGGATATGGAGTTGGACCTCAACAGTTAATGATAAACTAAT
GAGATTTTGATCACTGTGAGAAAGTTTACTGAAGTAGAAAAAAAGCTACAGCTTT
ATCACGTGGAAGCCTCAAAACTGGACCAAGAAATGCAGAACATTAAAAAGTTGCAGCT
ACTTGCAAGTGCAGTAAATGATTAAATGCAGATTAAATTCAAGTAGCCTTTCACCTG
TTCATTGACCTGGCAATTAAAGGTGTTAAATCTCCTGGTGTGATTTGACATAGATG
ATGCAAAGGTATTAGAATATTAAATGATCTGAAACAATATTGAAAAGAGGATATGGGTAT
ACTATTAACAGTCGATCCAGCTGCACCTGTTAGGATATCTTCAGCACTGGACAAAGC
AGTTGAACAGAAACAAAGGTCTCAGCAATTCTCCAGTCATCCTCCAGTTGGTCATG
CAGAGACTCTTCCACTGCTTCTCATGGCTACTCAAAGACAAGGAACCCCTAAC
GCGTACAATTACAAAAACAAATGCATCGGAAGTCCGAAGTGGTCTATTGTACCTTATGC
CTCGAACCTGATATTGTGCTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACATTCC
GAGTGCAGATGTTAAATGAAAAGGTGTTACCTTGGCTACTCACAAGAAACTGTTCA
TTTATGAAGATCTGAAGAACCACTACAAGGACATCCTCAGAGTTGTCAAACCAGTGAAGA
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGA**A**CT**G**TA**A**CTGAAGAACATT
AATTCTTAGGAATCTGAATGAGTGATTACATGCTGTAATAGGTAGGCAATTCTTGATT
ACAGGAAGCTTTATATTACTTGAGTATTCTGTCTTACAGAAAACATTGGGTTCTC
TCTGGGTTGGACATGAAATGTAAGAAAAGATTTCACTGGAGCAGCTCTTAAGGAGAA
ACAAATCTATTAGAGAAACAGCTGCCCTGCAAATGTTACAGAAATGAAATTCTCCTAC
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GGAGTAACAAATCTCAGTTGGACCACCTTAACCTGATTGAACACTGTCTAGGAAACTTAC
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TTGAAACAAGAAACAGAGTGTGAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA
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TTTACTCTAGGAAGTCTCAAAAGACCACCTTAAATTATTATGTTGGACAATTAGCAAC
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FIGURE 12

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RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCLFQDIFQHLDKAVEQKQRSQPISSPVLQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL
```

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACC_{CG}CGAC
TCCGGCTCTGCGCTCGGCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTGCATCATTACGGATT_{CG}
AGACAAGTACCCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGCGTGAATGACCGCAAGGAAATTGATGAGATGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGC_{CG}GAAGGCTGTACCACTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTTCACTGCTG
TTCACAAGGACGACTCTGGGAGTACTACTGCATTGCTTCAATGACCGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTTGCTGTACTGCCCTGA
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ACCCAGGGAAACCAGATGGAGTTAATCACATCCGCACTGACGAGGAGGGCAGTTCAGACACAAGTCATCGTTG
TGATCTGAAGCCCCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTAGAAACTCC_{TG}CAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAGCTTCTGTTGCCAAAGTTGACCA
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GGAAGGCAAAC_TGGGTGCGTTCACTGAGTTGGCTCTAATCTGTTCTGGCCTGATTCCCGATGAGTATTAGG
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GTAAATTGGTTGCTGGAAGAGGGATCTG_CCTGAGGAACCTGTTG_CCAACAGGGTGT_CAGGATTAAAGGAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTTCTGTTATTAAATTTAA
TACATCTAAATTGGCTAAGGATGTATTGATTATTGAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACAA_TGTTAAATAACCTATTGTTAAAAAGTTCAACTTAAGGTTAGAAGTCCAAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAAAGAGTATTGACCCAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTCT
CACACAAGTTTAGCCTTTCAACAGGAACTCATACTGTCACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCAGTTAAGCAATGTTGAAATCAGTTGCATCTCTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGTTGCGCCAGGC_{CCCC}CGCTAGCTCACTGTTG_CCTGCTG_CCCAGGAGGCCCT
GCCATCCTGGGCCCTGGCAGTGGCTGTG_{CC}CCAGTGAGCTTACTCACGTGCCCTGCTCATCCAGCACAGC
TCTCAGGTGGGACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCAGCTTGGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTACAAAATAGGGCCCCAATGCTATTGTTTAAGTTGTTAATTATTGTT
AAGATTGCTAAGGCCAAGGAATTGCGAAATCAAGTCTGTCAGTACAATAACATTTAAAGAAAATGGAT
CCCAC_TGTCTCTTGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTCGCAATTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGT_CAGGTGGAGCAGCAGGTAAGGCCTGGGGAGGAAAG
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCGAGACACTGCTCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAGCAAGGAAGGAGCTGCTGAGAAGGAGCACTCCACTGTG_CCTGGA
GAATGGCTCTCACTACTCACCTGTCTTCAGCTTCAAGTGTCTGGTTTTTAACTTGA_CAGCTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGAAACACTTGC_{CC}GCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTCTGTCATGGCATGGCATTGGATGCTTAGCATGCAAGTT
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCA_GCTCCAGCCTCCT
TCTTGGTTGTCAGTGTAGGGTAGCCTTATTGCCCTCTTCTTAAACCTCTACACTAGTGC_CATAACTGAGACTAGA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTACAGACTGCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATAGGAGCTGTGATTCT
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CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 14

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><subunit 1 of 1, 310 aa, 1 stop
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EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAGGTCTTACGCTGGAGCAGCGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
ATCCTGCTGACGCTGGCCCCCTCGAGCCGACGACAGCGAGTTCAGCGCTGGACATCTGGTTCCGGAG
GAGAAGCCACTGCCACCGCTTCTGGTGGACACATCGGAGGAGGCCTGCTGCTTCTGACTGGCTGAAGCTG
CGCATGATCGTTCTGAGGTGCTCCGCCTGGTGGACGCCCTGCAGGACCTGGAGCCGAGCAGCTGCTGCTG
TCGTGAGTCGTTGGATCCCCGTGTCAGCATGAGCAAACCTCCAGTTCTGGACCAGGCAGTGGCCAC
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCACCTGGTGGAGGTCCAGCATGAGC
GGCGCCTCCGGAGGCCAGACTTCACTCCTGTCACAGCCTCCCTGCCGCCCGAGACAGCACAGAGGCA
CCCAAACCAAAAGAGCAGCCCAGAGCAGGCCATAGGCCAGGGCCGGATTGGTGGGGACCCAGCTCCGGTGTG
GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTCGGCTCAGCCGGACCCCTCGGTGGCAGAGCTCC
AGTCCCCGCCCCGTGGCCCTGCCCTGCAGGCCCTGGCCAGGAGCTGGCCCGTGTCCAGGGCAGCCCC
GAGGTGCCGGCATCACGGTGTCTGCAGGCCCTGCCACCTGCTCAGCTCCCCACACGGCGGTGCCCTG
GTGATGTCCATGCACCGTAGCCACTTCTGGCTGCCCTGCTGCTGCCAGCTGCCAGTACCGCCTGTG
CCACAGGACACCGGCTTCTCGCTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGG
GTGGAGGGGGGGCTCCGTGCCCTGGCCAGGCCCTGGCCTTCGTCAAGGACCTGGAGGTGGTCAGCTCACCG
GTGCGAGGGGGGGCTCCGTGCCCTGGCCAGGCCCTGGCCTTCGTCAAGGACCTGGAGGTGGTCAGCTCACCG
CGTCCGTCATGCCACCTGAGGTCTGGGAGCAGTCAGCGTGGAGCCGGACTGATCAGCAAAGTCCCTCAG
GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTCTGCCACTGCGGATGCTGCC
TCCCCGTTCCAGCCTGTAAGCCCCTGGTGGTGGAGCTCCCTGCTGCAGGAGGAGGCCCTGGCTGG
GGGAAGCCGGGTGCCGACGGTGGCAGCCTGGAGGCCGTGGGCTGGGCCCTCGTCAAGGCCCTAGTGGACTGG
CTGGAAATGCTGGACCCGAGGTGGTCAGCAGCTGCCCGACCTGCAGCTCAGGCTGCTCTCTCCGGAGGAAG
GGCAAAGGTCAAGGCCAGGTGCCCTGTTCCGTCCTACCTCCTGACCCCTTCACGCATCAGTCCAGCTGGGCC
ACACTGCACCAGTCATCCGAGTCCTGCTGGCAAGAGCCGGAAACAGAGGTTGACCCCTCTGCTCTGGAC
TTCCTCTGGGCTGCATCCATGTTCTCGCATCTGGCAGGGGGGGGACCGAGCGCACCCCGCAGAAGCCGGGGAG
GAGCTGGTGTGGGGTCCAGGGCCGGAGCTCATCAGCCTGGTGGAGCTGATCTGGCCAGGCGGAGACGCGG
AGCCAGGACGGGGACACAGCCGCTGCAGCCTCATCCAGGCCGGCTGCCCTGCTGCTCAGCTGCTGTGG
GACGATGAGAGTGTCAAGGAAGGTGACGGAGCACCTGTCAGGCTGCATCCAGCAGTGGGAGACAGCGTGTGG
AGGCGCTGCCGAGACCTCTCTGCAGCTACAGCGGCCGGAGCTGGGGTGGCCCTGCTGAGGTCTTA
CTGCACAGCGAAGGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCAGCTCCTT
GCGGACACCAGCGACTCCCAGGGCTTGGAGAACCGAGGGGGGGGATGCCAGCATGCCCTGCCGAAGCTGGCGGT
GCGCACCCGCTGCTGCTCAGGCACCTGCCATGATCGGGCGCTCTGCACGGCCGACCCACCTCAACTTC
CAGGAGTTCCGGCAGCAGAACCCACCTGAGCTGCTTCTGCACGTGCTGGCCTGCTGGAGCTGCTGCAGCCGCAC
GTGTTCCCGAGCGAGCACAGGGGGCGCTGTGGGACTGCCTCTGCTCATCCGCTGCTGCTGAATTACAGG
AAGTCCCTCCGCCATCTGGCTGCTTCAACAAGTTGTGCAAGTTCATCCATAAGTACATTACATACAATGCC
CCAGCAGCCATCTCTTCTGCAGAAGCACGCCACCGCTCCAGCACCTGTCCTTCAGACAACAGTGACCTGGTG
ATGCTGAAATCCCTCTTGCAAGGCTCAGCCTGCCAGCAGGGAGCAGGACCGAGGCCCTGGACAGAG
GGCGAGGAGGAGAGCTCAGCCGGCTCTGGCCTCTGGTCAAGCGTCTCCCTGTTCACCCCTCTGACCGGGCCGAG
ATGGCCCCCTACATGAAACGGCTTCCCGGGCAAACCGTGGAGGATCTGCTGGAGGTCTGAGTGCACATAGAC
GAGATGTCAGGGGGAGACCCGAGATCCTGAGCTTCTCTGACCAACCTGCAGCGGCTGATGAGCTGGCCGAG
GAGTGTGCGCAACCTCGCCTTCAGCCTGGCCTGCGCTCATGAGAACAGCCAGCATTGCAAGCCGCTTTC
CTGCCACGTTCATGTAUTGCTGCTGGCAGCCAGGACTTGGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCGTG
TACGCTCTCTGTCGCAAGAGCACGCCAGGGCTGTGCTCCACGGGCCCTCTGGCATGACGCCAGATG
GACCCAGCGCAGATCTCGAGGCCCTGAGGATCTGCATATGGAGGCCGTGATGTGAGCTGTGGCAGCCGA
CCCCCTCCAAGCCCCGGCCGCTCCGGCCGGGATCTCGAGGCAAAGCCCAGGAAGCGTGGCGTTGCTGG
TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG
CTCGGGCCGGCCGCTGGCATAGGGCCGTCAGCAAGCCCTATTACACCTCTGGGCCACAGCCCTGCCGCG
AGCGGGGGATCCCCCGGGCATGGCCTGGCTGGTTGAATGAAACGACCTGAACGTCAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

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IRSEVLRLVDAALQDLEPQQLLLKVQSFVIPVSSMSKLLQFLDQAVAHDPTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPPIRDSTEAPPKPSSPEQPIGQGRIRVTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLQLCQYQRCVPQDTGFSSLFLKVLLQMLQWLDSPG
VEGGPLRQLRMLASQASAGRRLSDVRGGLLRAEALAFRQDLEVSVSSTRAVIATLRSGEQ
CSVEPDLISTKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSSLLLQEEPLA
GGKPGADGGSLEAVRLGPSSGLLVDWLEMPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIKVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTPKR
REELVLRVQGPTELISLVELILAEAEITRSQDGDTAACSLIQARLPLLLSCCCGDDESVRKVTE
HLSGCIQQQWGDSDLGRRCRDLQLQYLQRPELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVALAHPLLLRHPMIAALLHGRTHLNFQEFRQQNHL
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLNYRKSSRHLAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDEMSRRRPEILSFFSTNLQRL
MSSAEECCRNLAFSLALRSMQNPSIAAFLPTFMYCLGSQDFEVVQTALRNLPEYALLCQE
HAAVLLHRAFLVGMYQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGCAGCCTCGGCCCGCGGCCGCGCACCGAGGAGATGAGGCTCCGC
AATGGCACCTCCTGACGCTGCTCTCTGCCTGTGCGCCTCCTCGCTGTCTGGTA
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTACCAGCGGGAGTTCTGGCGC
TGCAGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA
TCGCACCTGGGCCGCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC
ACGTGCTGCACCTGCCAACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCAGCGGTGCGGTGGGCCAGGGCCGACCGGAGTGTGCGTGGTATGGCATCCC
GAGCGTGGCGCGAGGTGCACTGACTGACACTCTGACTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTATCGTGGTGCTGATGCCGAGACTGACTCACAG
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTGTTCCCACGGAGATCCATTCTGGCT
CCTGGAGGTCACTCACCCTCCCCCACTTCTACCCCTGACTTCTCCCGCTCCGAGAGTCCT
TTGGGGACCCCAGGGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC
ATGATGTACGCCAGTCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCAA
GCCCAACTACCTGAGCACCATGAAGAACCTTGCACTGCAGCAGCCTCAGAGGACTGGATGA
TCCTGGAGTTCTCCAGCTGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG
ATTGTAGAGTTCAATTCTCATGTTCTACCGGGACAAGGCCATCGACTGGCTCCTGGACCATAT
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAACGACTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTTCAAACCGTCCCTTCCAGCACGTGGCACTCACTCCTCGTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCAGCACTTACCCCTGGAGAAAG
CCTACCTGCGCGAGGACTTCTTCTGGCCTTCACCCCTGCCGGGGACTTCATCCGCTTC
CGCTTCTCCAACCTCTAACGACTGGAGCGTTCTTCTCGCAGTGGAACATCGAGCACCC
GGAGGACAAGCTCTCAACACGTCTGTGGAGGTGCTGCCCTCGACAACCCCTCAGTCAGACA
AGGAGGCCCTGCAGGAGGGCCGACCGCCACCCCTCCGGTACCCCTGGAGGCCGACGGCTAC
CTCCAGATCGGCTCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTCGGCC
TCTGGAAGCACTGCGCTCTCGATCCAGACGGACTCCCTGTGTGGTGATTCTGAGCGAGA
TCTTCTGAAAAAGGCCGACTAAAGCTGCGGGCTTCTGAGGGTACCCCTGTGGCCAGCCCTGAA
GCCACATTCTGGGGTGTGTCAGTGCCTCCCGAGGGCCAGATAACGGCCCCCCCCAA
AGGGTCTGCCTGGCGTGGGCTTGGGCCGCTGGGTCCGCCGCTGGCCGGAGGCCCTA
GGAGCTGGTGTGCCCCGCCGGCGAGGAGGCAGGGCCGGCCCCACACTGTGCC
TGAGGCCGGAACCGTTCGCACCCGGCTGCCCTGCCCCAGTCAGGCCGTTTAAAGAGCTTTAC
TTGGCGCCCGCCGTCTGGCGCAACACTGGAATGCATATACTACTTATGTGCTGTGTT
TTTATTCTGGATACATTGATTTTACGTAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAAATAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
MRLRNGTFLTLLLFCFLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRLHAAEQLRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLEDPRLKPNNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDESVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVWRWKQNLD
YCFLMMYAQSkgIYYVQLEDDIVAKPNLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDQDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFFSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAGPLEALRLSIQTDSPVWVILSEIFLKKAD
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Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515